Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1-13. (Cancelled)

14. (Currently Amended) ~~The method of claim 13,~~ A method of associating a phenotype with one or more candidate chromosomal regions in a genome of a species using a phenotypic data structure that comprises a difference in a phenotype between different strains of said species, said genome including a plurality of loci, said method comprising:

establishing a genotypic data structure, said genotypic data structure corresponding to a locus in said plurality of loci, said genotypic data structure comprising a variation of at least one component of said locus between different strains of said species;

comparing said phenotypic data structure to said genotypic data structure to form a correlation value; and

repeating said establishing and comparing steps for each locus in said plurality of loci, thereby identifying one or more genotypic data structures that form a high correlation value relative to all other genotypic data structures that are compared to said phenotypic data structure by said comparing step; wherein the loci that correspond to said one or more genotypic data structures that form a high correlation value represent said one or more candidate chromosomal regions and wherein an amount of said genome that is included in each locus in said plurality of loci is predetermined; wherein

each element in said genotypic data structure corresponds to a difference of at least one component of said locus between different strains of said species; wherein, for each element in said genotypic data structure, said different strains of said species are selected from a plurality of strains of said species;

an amount that a variation contributes to said at least one component of said locus between different strains of said species is a function of a distance said variation is away from a center of the locus that corresponds to said genotypic data structure; and

wherein said genotypic data structure comprises a plurality of variations that are distributed about the center of said locus, and said establishing step further comprises:

fitting a distribution of said plurality of variations about the center of said locus with a probability function; and

weighting each variation by a corresponding value derived from said probability function such that variations further from the center of said locus are downweighted so that they contribute less to said genotypic data structure than loci that are closer to said center of said locus.

15. (Original) The method of claim 14 wherein said probability function is a Gaussian probability distribution, a Poisson distribution, or a Lorentzian distribution.

16. (Cancelled)

17. (Currently amended) ~~The method of claim 1,~~ A method of associating a phenotype with one or more candidate chromosomal regions in a genome of a species using a phenotypic data structure that comprises a difference in a phenotype between different strains of said species, said genome including a plurality of loci, said method comprising:

establishing a genotypic data structure, said genotypic data structure corresponding to a locus in said plurality of loci, said genotypic data structure comprising a variation of at least one component of said locus between different strains of said species;

comparing said phenotypic data structure to said genotypic data structure to form a correlation value; and

repeating said establishing and comparing steps for each locus in said plurality of loci, thereby identifying one or more genotypic data structures that form a high correlation value relative to all other genotypic data structures that are compared to said phenotypic data structure by said comparing step; wherein the loci that correspond to said one or more genotypic data structures that form a high correlation value represent said one or more candidate chromosomal regions and wherein an amount of said genome that is included in each locus in said plurality of loci is predetermined; wherein,

said correlation value is formed in accordance with the expression:

$$c(P, G^L) = \frac{\Sigma^i (p(i) - < P >) \ (g(i) - < G^L >)}{\{[\Sigma^i (p(i) - < P >)^2] [\Sigma^i (g(i) - < G^L >)^2]\}^{1/2}}$$

where,

$c(P, G^L)$ is said correlation value;

p(i) is a value of the i^{th} element of said phenotypic data structure;

g(i) is a value of the i^{th} element of said genotypic data structure;

$<P>$ is a mean value of all elements in said phenotypic data structure; and

$<G^L>$ is a mean value of all elements in said genotypic data structure.

18-19. (Cancelled)

20. (Currently amended) ~~The method of claim 1,~~ A method of associating a phenotype with one or more candidate chromosomal regions in a genome of a species using a phenotypic data structure that comprises a difference in a phenotype between different strains of said species, said genome including a plurality of loci, said method comprising:

establishing a genotypic data structure, said genotypic data structure corresponding to a locus in said plurality of loci, said genotypic data structure comprising a variation of at least one component of said locus between different strains of said species;

comparing said phenotypic data structure to said genotypic data structure to form a correlation value; and

repeating said establishing and comparing steps for each locus in said plurality of loci, thereby identifying one or more genotypic data structures that form a high correlation value relative to all other genotypic data structures that are compared to said phenotypic data structure by said comparing step; wherein the loci that correspond to said one or more genotypic data structures that form a high correlation value represent said one or more candidate chromosomal regions and wherein an amount of said genome that is included in each locus in said plurality of loci is predetermined; wherein,

said correlation value is formed in accordance with the expression

$$c(P, G^L) = \frac{[\Sigma^i (p(i) - <P>)\ (g(i) - <G^L>)] \times \mathbf{Z}}{\{[\Sigma^i (p(i) - <P>)^2]\ [\Sigma^i (g(i) - <G^L>)^2]\}^{1/2}}$$

where,

$c(P, G^L)$ is said correlation value;

p(i) is a value of the i^{th} element of said phenotypic data structure;

g(i) is a value of the i^{th} element of said genotypic data structure;

$<P>$ is a mean value of all elements in said phenotypic data structure;

$<G^L>$ is a mean value of all elements in said genotypic data structure; and
Z is a function of a number of components in said locus having a variation between different strains of said species.

21. (Original) The method of claim 20, wherein said function is selected from the group consisting of taking the square root of Z, squaring Z, raising Z by the power of a positive integer, taking a logarithm of Z, and taking an exponential of Z.

22. (Currently amended) ~~The method of claim 1,~~ A method of associating a phenotype with one or more candidate chromosomal regions in a genome of a species using a phenotypic data structure that comprises a difference in a phenotype between different strains of said species, said genome including a plurality of loci, said method comprising:

establishing a genotypic data structure, said genotypic data structure corresponding to a locus in said plurality of loci, said genotypic data structure comprising a variation of at least one component of said locus between different strains of said species;

comparing said phenotypic data structure to said genotypic data structure to form a correlation value; and

repeating said establishing and comparing steps for each locus in said plurality of loci, thereby identifying one or more genotypic data structures that form a high correlation value relative to all other genotypic data structures that are compared to said phenotypic data structure by said comparing step; wherein the loci that correspond to said one or more genotypic data structures that form a high correlation value represent said one or more candidate chromosomal regions and wherein an amount of said genome that is included in each locus in said plurality of loci is predetermined; wherein,

said correlation value is a correlative measure cm that is computed in accordance with the expression:

$$cm(P, G^L) = \frac{[\Sigma^i (p(i) - <P>)\ (g(i) - <G^L>)]}{\{[\Sigma^i (p(i) - <P>)^2]\}^{1/2}}$$

where,

$cm(P, G^L)$ is said correlative measure;

p(i) is a value of the i^{th} element of said phenotypic data structure;

g(i) is a value of the i^{th} element of said genotypic data structure;

$\langle P \rangle$ is a mean value of all elements in said phenotypic data structure; and

$\langle G^L \rangle$ is a mean value of all elements in said genotypic data structure.

23-38. (Cancelled)

39. (Currently amended) ~~The computer program product of claim 26,~~ A computer program product for use in conjunction with a computer system, the computer program product comprising a computer readable storage medium and a computer program mechanism embedded therein, the computer program mechanism comprising:

a genotypic database for storing variations in genomic sequences of a plurality of strains of a species;

a phenotypic data structure, said phenotypic data structure comprising a difference in a phenotype between different strains of said species; and

a program module for associating a phenotype with one or more candidate chromosomal regions in a genome of said species, said genome including a plurality of loci, said program module comprising:

instructions for establishing a genotypic data structure, said genotypic data structure corresponding to a locus in said plurality of loci, said genotypic data structure comprising a variation of at least one component of said locus between different strains of said species stored in said genotypic database;

instructions for comparing said phenotypic data structure to said genotypic data structure to form a correlation value; and

instructions for repeating said instructions for establishing and said instructions for comparing, for each locus in said plurality of loci, thereby identifying one or more genotypic data structures that form a high correlation value relative to all other genotypic data structures that are compared to said phenotypic data structure by said instructions for comparing; wherein the loci that correspond to said one or more genotypic data structures that form a high correlation value represent said one or more candidate chromosomal regions and wherein an amount of said genome that is included in each locus in said plurality of loci is predetermined; wherein, said genotypic data structure represents a plurality of variations that are distributed about the center of said locus, and said instructions for establishing further comprise:

instructions for fitting a distribution of said plurality of variations about the center of said locus with a probability function; and

instructions for weighting each variation by a corresponding value derived from said probability function such that variations further from the center of said locus are downweighted so that they contribute less to said genotypic data structure than loci that are closer to said center of said corresponding locus.

40. (Original) The computer program product of claim 39 wherein said probability function is a Gaussian probability distribution, a Poisson distribution, or a Lorentzian distribution.

41. (Cancelled)

42. (Currently amended) ~~The computer program product of claim 26~~ A computer program product for use in conjunction with a computer system, the computer program product comprising a computer readable storage medium and a computer program mechanism embedded therein, the computer program mechanism comprising:

a genotypic database for storing variations in genomic sequences of a plurality of strains of a species;

a phenotypic data structure, said phenotypic data structure comprising a difference in a phenotype between different strains of said species; and

a program module for associating a phenotype with one or more candidate chromosomal regions in a genome of said species, said genome including a plurality of loci, said program module comprising:

instructions for establishing a genotypic data structure, said genotypic data structure corresponding to a locus in said plurality of loci, said genotypic data structure comprising a variation of at least one component of said locus between different strains of said species stored in said genotypic database;

instructions for comparing said phenotypic data structure to said genotypic data structure to form a correlation value; and

instructions for repeating said instructions for establishing and said instructions for comparing, for each locus in said plurality of loci, thereby identifying one or more genotypic data structures that form a high correlation value relative to all other genotypic data structures that are compared to said phenotypic data structure by said instructions for comparing;

wherein the loci that correspond to said one or more genotypic data structures that form a high correlation value represent said one or more candidate chromosomal regions and wherein an amount of said genome that is included in each locus in said plurality of loci is predetermined; wherein, said instructions for comparing include instructions for forming said correlation value in accordance with the expression:

$$c(P, G^L) = \frac{\Sigma^i (p(i) - < P >) \ (g(i) - < G^L >)}{\{[\Sigma^i (p(i) - < P >)^2] [\Sigma^i (g(i) - < G^L >)^2]\}^{1/2}}$$

where,

$c(P, G^L)$ is said correlation value;

$p(i)$ is a value of the i^{th} element of said phenotypic data structure;

$g(i)$ is a value of the i^{th} element of said genotypic data structure;

$<P>$ is a mean value of all elements in said phenotypic data structure; and

$<G^L>$ is a mean value of all elements in said genotypic data structure.

43- 44. (Cancelled)

45. (Currently amended) ~~The computer program product of claim 26~~, A computer program product for use in conjunction with a computer system, the computer program product comprising a computer readable storage medium and a computer program mechanism embedded therein, the computer program mechanism comprising:

a genotypic database for storing variations in genomic sequences of a plurality of strains of a species;

a phenotypic data structure, said phenotypic data structure comprising a difference in a phenotype between different strains of said species; and

a program module for associating a phenotype with one or more candidate chromosomal regions in a genome of said species, said genome including a plurality of loci, said program module comprising:

instructions for establishing a genotypic data structure, said genotypic data structure corresponding to a locus in said plurality of loci, said genotypic data structure comprising a variation of at least one component of said locus between different strains of said species stored in said genotypic database;

instructions for comparing said phenotypic data structure to said genotypic data structure to form a correlation value; and

instructions for repeating said instructions for establishing and said instructions for comparing, for each locus in said plurality of loci, thereby identifying one or more genotypic data structures that form a high correlation value relative to all other genotypic data structures that are compared to said phenotypic data structure by said instructions for comparing; wherein the loci that correspond to said one or more genotypic data structures that form a high correlation value represent said one or more candidate chromosomal regions and wherein an amount of said genome that is included in each locus in said plurality of loci is predetermined, wherein said instructions for comparing include instructions for forming said correlation value in accordance with the expression:

$$c(P, G^L) = \frac{[\Sigma^i (p(i) - < P >) \ (g(i) - < G^L >)] \times \mathbf{Z}}{\{[\Sigma^i (p(i) - < P >)^2] [\Sigma^i (g(i) - < G^L >)^2]\}^{1/2}}$$

where,

$c(P, G^L)$ is said correlation value;

$p(i)$ is a value of the i^{th} element of said phenotypic data structure;

$g(i)$ is a value of the i^{th} element of said genotypic data structure;

$<P>$ is a mean value of all elements in said phenotypic data structure;

$<G^L>$ is a mean value of all elements in said genotypic data structure; and

Z is a function of a number of components in said locus having a variation between different strains of said species.

46. (Currently amended) ~~The computer program product of claim 43,~~ A computer program product for use in conjunction with a computer system, the computer program product comprising a computer readable storage medium and a computer program mechanism embedded therein, the computer program mechanism comprising:

a genotypic database for storing variations in genomic sequences of a plurality of strains of a species;

a phenotypic data structure, said phenotypic data structure comprising a difference in a phenotype between different strains of said species; and

a program module for associating a phenotype with one or more candidate chromosomal regions in a genome of said species, said genome including a plurality of loci, said program module comprising:

instructions for establishing a genotypic data structure, said genotypic data structure corresponding to a locus in said plurality of loci, said genotypic data structure comprising a variation of at least one component of said locus between different strains of said species stored in said genotypic database;

instructions for comparing said phenotypic data structure to said genotypic data structure to form a correlation value; and

instructions for repeating said instructions for establishing and said instructions for comparing, for each locus in said plurality of loci, thereby identifying one or more genotypic data structures that form a high correlation value relative to all other genotypic data structures that are compared to said phenotypic data structure by said instructions for comparing; wherein the loci that correspond to said one or more genotypic data structures that form a high correlation value represent said one or more candidate chromosomal regions and wherein an amount of said genome that is included in each locus in said plurality of loci is predetermined, wherein

said correlation value is weighted by a number of components in said locus; and

~~wherein~~ said function is selected from the group consisting of taking the square root of Z, squaring Z, raising Z by the power of a positive integer, taking a logarithm of Z, and taking an exponential of Z.

47. (Currently amended) ~~The computer program product of claim 26,~~ A computer program product for use in conjunction with a computer system, the computer program product comprising a computer readable storage medium and a computer program mechanism embedded therein, the computer program mechanism comprising:

a genotypic database for storing variations in genomic sequences of a plurality of strains of a species;

a phenotypic data structure, said phenotypic data structure comprising a difference in a phenotype between different strains of said species; and

a program module for associating a phenotype with one or more candidate chromosomal regions in a genome of said species, said genome including a plurality of loci, said program module comprising:

instructions for establishing a genotypic data structure, said genotypic data structure corresponding to a locus in said plurality of loci, said genotypic data structure comprising a

variation of at least one component of said locus between different strains of said species stored in said genotypic database;

instructions for comparing said phenotypic data structure to said genotypic data structure to form a correlation value; and

instructions for repeating said instructions for establishing and said instructions for comparing, for each locus in said plurality of loci, thereby identifying one or more genotypic data structures that form a high correlation value relative to all other genotypic data structures that are compared to said phenotypic data structure by said instructions for comparing; wherein the loci that correspond to said one or more genotypic data structures that form a high correlation value represent said one or more candidate chromosomal regions and wherein an amount of said genome that is included in each locus in said plurality of loci is predetermined, wherein,

said instructions for comparing include instructions for forming said correlation value in accordance with a correlative measure cm that is computed in accordance with the expression:

$$cm\,(P, G^L) = \frac{[\Sigma^i\,(p(i) - \langle P \rangle)\;\;(g(i) - \langle G^L \rangle)]}{\{[\,\Sigma^i\,(p(i)\;\; - \langle P \rangle)^2]\,\}^{1/2}}$$

where,

cm (P, G^L) is said correlative measure;

p(i) is a value of the i^{th} element of said phenotypic data structure;

g(i) is a value of the i^{th} element of said genotypic data structure;

$\langle P \rangle$ is a mean value of all elements in said phenotypic data structure; and

$\langle G^L \rangle$ is a mean value of all elements in said genotypic data structure.

48-57. (Cancelled)

58. (Currently amended) ~~The computer system of claim 52,~~ A computer system for associating a phenotype with one or more candidate chromosomal regions in a genome of a species, said genome including a plurality of loci, the computer system comprising:

a central processing unit;

a memory, coupled to the central processing unit, the memory storing:

a genotypic database for storing variations in genomic sequences of a plurality of strains of said species;

a phenotypic data structure that comprises a difference in a phenotype between different strains of said species; and

a program module, said program module comprising:

instructions for establishing a genotypic data structure, said genotypic data structure corresponding to a locus in said plurality of loci, said genotypic data structure comprising a variation of at least one component of said locus between different strains of said species stored in said genotypic database;

instructions for comparing said phenotypic data structure to said genotypic data structure to form a correlation value; and

instructions for repeating said instructions for establishing and said instructions for comparing, for each locus in said plurality of loci, thereby identifying one or more genotypic data structures that form a high correlation value relative to all other genotypic data structures that are compared to said phenotypic data structure by said instructions for comparing; wherein the loci that correspond to said one or more genotypic data structures that form a high correlation value represent said one or more candidate chromosomal regions and wherein an amount of said genome that is included in each locus in said plurality of loci is predetermined, wherein said instructions for comparing include instructions for forming said correlation value in accordance with the expression:

$$c(P, G^L) = \frac{\Sigma^i (p(i) - \langle P \rangle)\ (g(i) - \langle G^L \rangle)}{\{[\Sigma^i (p(i) - \langle P \rangle)^2]\ [\Sigma^i (g(i) - \langle G^L \rangle)^2]\}^{1/2}}$$

where,

$c(P, G^L)$ is said correlation value;

$p(i)$ is a value of the i^{th} element of said phenotypic data structure;

$g(i)$ is a value of the i^{th} element of said genotypic data structure;

$\langle P \rangle$ is a mean value of all elements in said phenotypic data structure; and

$\langle G^L \rangle$ is a mean value of all elements in said genotypic data structure.

59-77. (Cancelled)